

ORF2 Sequencing



Chromatogram quality evaluation



Alignment with reference sequences
(Codon level; e.g. TranslatorX)



Reduced dataset
(Fig. 2)
(Fast)

Complete dataset
(Supplementary data)
(Accurate)



Neighbor joining tree
(p-distance; bootstrap support)
ClusterPicker cluster evaluation



Intra cluster distance <13%
Bootstrap support >70



Yes

No



Previously
described
genotype

Compare with updated
Genbank records



New cluster
bootstrap support >70
& >15 sequences



Yes

No



New genotype

Unclassified